

OM of: US-09-303-518D-569 to: Issued_Patents_AA:* out_format : pfs
Date: Jun 30, 2002 6:55 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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Search information block:

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Query length: 897
Database: Issued_Patents_AA:*
Database sequences: 231628
Database length: 24425594
Search time (sec): 185.890000

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seq documentation block:

: Sequence 2, Application US/08926636

: Patent No. 6080949

: GENERAL INFORMATION:

: APPLICANT: Bernudes, David

: APPLICANT: Low, Kenneth

: TITLE OF INVENTION: Mutant Salmonella msds

: NUMBER OF SEQUENCES: 4

: CORRESPONDENCE ADDRESSES:

: ADDRESSEE: Pennie & Edmonds LLP

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1 STREET: 1155 Avenue of the Americas
2 City: New York
3 STATE: New York
4 COUNTRY: USA
5 ZIP: 10036-2711
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: diskette
8 COMPUTER: IBM compatible
9 OPERATING SYSTEM: DOS
10 SOFTWARE: Fastseq Version 2.0
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/926,636
13 FILING DATE:
14 CLASSIFICATION: 436
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Baldwin, Geraldine F.
17 REGISTRATION NUMBER: 31,232
18 REFERENCE/DOCKET NUMBER: 8002-038
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (212) 790-9090
21 TELEFAX: (212) 869-8864
22 TELE: 6614 PENNIE
23 INFORMATION FOR SEQ ID NO: 2:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 323 amino acids
26 TYPE: amino acid
27 STRANDEDNESS:
28 TOPOLOGY: unknown
29 MOLECULE TYPE: protein
30 US-08-926-636--2

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Percent Identity: 24.138

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; Patent No. 6355411
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; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
;
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
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; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
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227 ySgIyAlaAlaArg.....GlyArg..... 233
201 TCCCGACCCCAAAACGGTCAAGCGCTTTTGGGAAACGGCAAAAGCG 250
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401 GCGGACGCTACATCAGCAGCAGCTTCCTCCGCTGACCGCCATGTAC 450
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319 LeuProLeuProGlyLysArgProAlaGlyLysHisAlaGlyAlaAr 335
497 G.....GGTTCGGCGCAAGGAAAGAAACCGCGCTACACGATCAAGGG 540
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; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIOLENCE-ASSOCIATED NUCLEIC ACID
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-277

```

alignment_scores:

Quality: 112.50 Length: 382
Ratio: 0.771 Gaps: 16
Percent Similarity: 38.220 Percent Identity: 22.513

alignment block:

US-09-303-518D-569 x US-09-199-637A-277 ..

Align seg 1/1 to: US-09-199-637A-277 from: 1 to: 558

```

18 CAGCGTGTTCCTCCCTTTGCGAAGCGCCATGCA.....CA 52
   ||||| ||||| ||||| |||
17 GlnAlaValAlaProLeuHisHisArgSerAlaThrAlaGlyGlnGly 33
53 TCCTGTTCACCGCCCTGCTCAAAATGCTCTCCCTGCTGCGCTTTCCTGT 102
   ||||| ||||| ||||| |||
33 sArgProAspArgArgGlyArgGlnProHisProHisGlyAspArgLeuG 50
103 CTGCA.....CAGCGTGGGAACCGCGCTGCGACA 131
   ||||| ||||| ||||| |||
50 LysAlaGlyLysThrGlySerSerArgProSerProAspProAlaLysP 66
132 TCTGGCGTTTACCTTTTAAGGAAGACCGCGCGCATCGCGC..... 176
   ||||| ||||| ||||| |||
67 ArgAlaArgGlyAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 83
177 ....CAATATGCGCTCAGCGCAGCATGATCCGACCC..... 209
   ||||| ||||| ||||| |||
83 oGlyGlnAlaGlyGlyGlyTyLArgGlnAlaArgAlaArgLysArgArgP 100
209 ..... 209
100 rArgGlyAspLeuGlnValArgGlnGlyArgGlyAlaGlyLeuGlyAla 116
210 .....CAAAAGGTCAAGCGCTTTTGGCG 235
   ||||| ||||| ||||| |||
117 AspProAlaGlnAspArgAlaGlyGlnAlaGlyAspGlyGlyAlaAl 133
236 AAACGGCAAAAGCGCGTTT..... 254

```

```

133 aGlnGlyArProArGlnHisGlyAlaHisProValProAspHisProG 150
255 .....GGAAGTGGCCCGCGTTTTCAGAAACCGGAGACATAGAAAC 299
      ||||| |||
150 LyrProGlyThrGlnProAlaAspGlyArGProAlaArGlnAspArgGlu 166
      |||
300 AATGTT.....CAAAGCGGTACAGCGCTGGGAACATGTGACAGCGCTT 343
      |||
167 ProValAlaAlaGlnGlnGlnLysPArgArgGlyLysnArGArgSerGlyPh 183
      |||
344 T.....GGACAAACAGGAA 357
183 eGlnValAspArgTyrProGlyValGlnAspAlaArgGlyValArgAlaArg 200
358 GGGCGCTATTATCATCAGCC..... 377
200 LuAlaAlaAlaHisGlyAlaGlyAlaAlaSerAlaSerAspArgProGly 216
378 .....GCACATCGCAGCTACGATTGGCGCGAGCGCT 409
217 ArgGlyGlySerArgArgValGlnArgArgAlaProPheAlaArg..... 231
410 ACATCAGCGCAGAGCTCCGTCGCGTACCGCGCATGTACAAACCGCGC 459
      |||
232 ...ArgProArGArgSerGlnProAlaGlnArgLeuValProLeuProA 247
460 AAATCAAGGCGATAGACAAAT..... 482
247 rGProAspArgGlyGlnAspArgValValGlnGlyAlaGlyArgVal 263
483 .....CATGCAGCGCGGCGGCTCGCGGCAAGGAAAAACCGCGC 523
264 ProLeuArGlyArgGlyGlyAlaGlyAlaAspArg..... 275
524 CTACAGCATACAAAGGCGTCAAAACATCAACAAAGCGCTTCGGCGC 573
      |||
276 TyValArgValHisGlyGlnThrLeuGlyLysProProAspArgArg 292
574 GAAGCACCATCGTCTGCTCCGACACAGTCCCTCCCTCAGA..... 617
      |||
292 lAsArgGlyLeuArGArgLeuArgGlyArgArgLeuProAspArgGlyAsp 308
618 .....AGGCGGGAAGCGCTATGCGTGATG 643
309 ProProGlnAlaLeuLeuGlyGlyAlaAlaGlyArg.....GlyGlyG1 323
644 TCTTGGCAACCTGCTATACATGACGTGCGGCGCAAAATTTGGCACAC 693
      |||
323 uGlyProSerGlyCysTLeuHisSerProProGlyAlaArgGly.... 338
694 GTCAAGGCGTGAAGAACCTGTTTCTGCTCGCAAGCGCTGCGCGG 743
339 .....ArgThrProAspArgGln 344
744 ACAAGGTT..... 752
345 SerArgAlaTyrGlyGlyLeuProGlnHisArgGlyGlyAspAspLeuG1 361
753 .....CGATTTCACATCCGCC.....CGTCCAAAGGGA 782
361 nProArGpHeGlyAlaAspProGlyAlaGlyArgArgProArgGly 376
seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-327-832-5
seq_documentation_block:
; Sequence 5, Application US/08327832
; Patent No. 5840832
; GENERAL INFORMATION:
; APPLICANT: Ono, Santa J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: Transcription Factor Regulating MHC
; TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
; TITLE OF INVENTION: Retroviral Expression Constructs Thereof

```

```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,832
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fosorste, Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107,46362
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9153
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-832-5

```

```

alignment_scores:
      Quality: 112.00      Length: 368
      Ratio: 0.848      Gaps: 18
      Percent Similarity: 35.870      Percent Identity: 20.380

```

```

alignment_block:
US-09-303-518D-569 x US-08-327-832-5

```

```

Align seg 1/1 to: US-08-327-832-5 from: 1 to: 1104

```

```

14 AATTGAGGCTGTTCCCTTTGCGAAGC...CCATGCACATCTCT.. 58
      ||| |||
553 AsnHisThrCysSerGlnValCysHisProGlnProCysGlnGlnCysPr 569
59 .....TGACGCGCCCTGCTCAATGACCTCTCCCTGTCGCTTCTCTGCT 104
      |||
569 cArgLeuProGlnLeuValArgCysCysProCysGlnGlnThrProLeus 586
105 GCACAGCGTGGGAACCGGCTCGGACATCTGGCGTTTACCTTTAAAG 154
586 eGlnLeuLeuGlnLeuGlySerSer.....Arg 596
155 AAAGCGCGCGCGCATCGTCGCCAATATGCGTCAGGCAAGCATGAAATCC 204
      |||
597 LysThrCysMetAspProValProSerCysGlyLysValCysGlyLysPr 613
205 GACCCCAAAACGCTCAAGACCGTTTTCGGGAACGCAAAAGCGGTTT 254
      |||
613 cLeuProCysGlySerLeuAspPheLe..... 622
255 GGAACCTTGCCCGCGCGTTTTCAGAAAACGGAAGACATAGAACAAAGT 304
622 ..... 622
305 TCAAGCGGTACACGCGCTGGAAACATGTGCACAGCGTTTGGACAAACAC 354
      |||
623 .....HisThrCysGlnLysLeuCys.....HisG1 631
355 GAAGGCTGCTATTATTCACGCGCGCACATCGGCGAGCGATGATTGGCGG 404
      |||

```

```

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
City: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,584
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.46362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9153
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-584-5

alignment_scores:
Quality: 112.00 Length: 368
Ratio: 0.848 Gaps: 18
Percent Similarity: 35.870 Percent Identity: 20.380

alignment_block:
US-09-303-518D-569 x US-08-828-584-5 ..

Align seg 1/1 to: US-08-828-584-5 from: 1 to: 1104

14 AATTCAGGCGTGTTCCTCCCTTGGCGAACG...CCATGCACATCCTGT.. 58
||| ||| :::::|||| ||||| :::::|||
553 AsnHlStHnrcysserGlnValCysHisProGlnProCysGlnGlnCysPr 569
59 ...TGACCGCCCTGCTCAAAATGCCCTCCCTGCTGCCCGCTTCTCTGT 104
||| ::::: ||||| ::: ||:::
569 oArgLeuProGlnLeuValArgCysCysProCysGlyGlnThrProLeus 586
105 GCACACGCTGGGAACCGCGCTGGCACATCGCGCTTTTACCTTTAAAG 154
||| ||| |||||::: Arg 596
586 eArgLeuLeuLeuIleuGlySerSer.....Arg 596
155 AAGACGCGCGCGCATCGTCGCATATATGCGTCAGCAGCAGCATGATGCC 204
|||||::: ||| ||| ::: ::: |||
597 LysThrCysMetAspProValProSerCysGlyValCysGlyLysPr 613
205 GACCCCAAAACGGTCAAAAGCCGTTTTCGGAACGCGCAAAAGCGGTTT 254
| ||| ||| ||:::
613 oLeuProCysGlySerLeuAspPheIle..... 622
255 GGAACCTTGCCCCCGGCTTTTCAGAAACCGGAAGACATVAGAACAAVTGT 304
622 ..... 622
305 TCMAAGCGGTACACGCGTGGGAACATGTGCACAGCGCTTTGGACAAACAC 354
:::||||::: :::::|||
623 .....HisThrCysGlnLysLeucys .....HisG1 631
355 GAAGGCGTGTATTTCATCAGCGCCACATCGGCAAGCTACGATTTGGGCGG 404
||| ||||| |||||:::

```

[illegible]

```

: APPLICANT: Cino, Paul M
: APPLICANT: Dougherty, Brian A
: APPLICANT: Goldberg, Steven L
: APPLICANT: Hofle, Gerhard
: APPLICANT: Mueller, Joachim
: APPLICANT: Reichenbach, Hans
: TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or
: TITLE OF INVENTION: heteropolypeptide compounds
: FILE REFERENCE: PCT/US 99/2535
: CURRENT FILING DATE: 1999-10-07
: EARLIER APPLICATION NUMBER: DE 198 46 493.2
: EARLIER FILING DATE: 1998-10-09
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 78
: LENGTH: 882
: TYPE: PRT
: ORGANISM: Sorangium cellulosum
US-09-413-814-78

alignment_scores:
      Quality: 109.00      Length: 340
      Ratio: 0.826      Gaps: 14
      Percent Similarity: 38.824      Percent Identity: 25.294

alignment_block:
US-09-303-518D-569 x US-09-413-814-78 ..

Align seg 1/1 to: US-09-413-814-78 from: 1 to: 882

48 GCACATCCTGTTGACCGCCGCTGCTCAATGCGTCTC.....CCTGC 88
   ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
464 ALaasprProIarGargPrOalPrOalValValaLargAlaAlaPrOal 480
   TCGCGGTTTCGTCMGACAAGCGGGAAA..... 119
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 aValValaLargargSerAlaLargAlaGlyGlnProGlyValaGlnHisProV 497
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
120 .....CGCGTCGACATCTGCGGTTTTCACCTTTT 149
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
497 aLargGlyAlaLargaspGlyProAlaLargargArgAlaPrOProGln 513
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
150 AAAGAGACCGCGCGCATCGTCGCAATATGCGTCAGCGACGATCA 199
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
514 PrOValaLargaspArgAlaAlaPrOarg.....GlyAlaAlaAs 526
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 ATCCCGACCCCAAAAGCGTCAAAGCCGTTTTCGGAACGCGCAAAAGCC 249
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
526 pspsAlaGlnargGlnGlyArgargAlaValaPrOglArgargAlaArgG 543
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 GATTGGAACTGCGCCCGCGTTTTCAGAAACGCGAAGCATAGAAC 299
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
543 LpProGlyAlaValaPrOaspValaLargPrOalGAlaPrOalGlyArgGly 559
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 AATGTTCAAGCGGT..... 314
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
560 PrOalArgargGlyGlyLeuGlyAlaLargPrOalrGlyGlyPrOalrAlaVa 576
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
315 .....ACAGCGTCGGACATCTGCAAGCATGTTTTCGACAAACAC 354
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
576 LArgPrOgluprOalrGAlaAlaPrOPrOalrGAlaHisPrOgluAlaP 593
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
355 GAAGGCGCTATTTCATCAGCGC.....GCACATCGGCACACTAGA... 395
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
593 rOalrGAlaLargHisLargAlaLargargAlaPrOalrGargValaLargarg 609
   ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
396 ...TTTGGCGGACGCTACATCAG..... 416
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
610 LeuValGlyLargargLeuLargargAlaLargargAlaLeuAlaGargLe 626
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
417 .....CCAGACGCTTCGTTCCGCGTGAACCGGCATG 447

```

```

US-09-413-814-79

alignment_scores:
  Quality: 109.00      Length: 328
  Ratio: 0.762        Gaps: 17
  Percent Similarity: 43.598      Percent Identity: 26.524

alignment_block:
US-09-303-518D-569 x US-09-413-814-79      ..
Align seg 1/1 to: US-09-413-814-79 from: 1 to: 1213

```

```

Align seg 1/1 to: US-09-413-814-79 from: 1 to: 1213

27 TCCSCCCTTTGCGAAGCCGATGCAATCCTGTTGACCCGCTCTCAAT 76
   ::::: ::::: ||| ||| ||| ||| ||| ||| ||| |||
356 AATPCHIsAsrPrgtAgtAlaIaValGlnAsPrgtAgtProB1yPrg 372
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
77 GCGTCGCCCTGCGCGCGCTTCTGTCGTGCAAGCGGTGGGAACCGCTC 126
   : ||| : ::::: ||| : ::::: ||| : ::::: ||| :
372 u...LeuAgtAgtAgtAsPrgIsAgtAlaIaValAlaHisAgtPro 388
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
127 GCACATCTGGCGTTTACCTTTT.....AAGCAAGACCG 161
   ::::: ||||| ::::: ::::: ||||| |||||
388 LglnAsPrgtAgtLeuPrgtPrgtHisAgtAlaAgtAgtAsPrgtAgt 404
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
162 CGCGCGCATGCTGCCAATATGCGTCGGAGGCGCATGATCCGACCCCA 211
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
405 ArgAlaIaProLeuGltAgtAlaIaGltAgt..... 415
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
212 AACGCGTCAAGCCGTTTTCGGA..... 236
   ::::: ||| ::::: ::::: ::::: ::::: ::::: :::::
416 .GltGltAgtAsPrgtAgtAgtAlaIaGltAgtAlaProGltAgtAla 432
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
237 ..AAGCGCAAAAGCGGTTTGGAACTGCCCCCGCTTTTCAGAAAAC 284
   ::::: ::::: ||||| ::::: ::::: ||||| ::::: :::::
432 rgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgt 448
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
285 GGAAGACATAGAAACAATGTTCAAGCGGTACAGCGCTGGACATGTGC 334
   ::::: ::::: ::::: ::::: ||| ::::: ::::: :::::
449 ALaIaGltAgtAlaHisAsPrgtAgtGltAgtAgtAgtProPrgtAla 465
   ::::: ::::: ::::: ::::: ||||| ||||| ||||| :::::
335 AGCA.....GGCTTGGACAACACCGAAGGCGCTCTTATCATCAG 375
   ||||| ::::: ::::: ::::: ::::: ||||| ||||| :::::
465 aAlaGltAgtAlaIaGltAgtAlaGltAgtProAgtAgtProAlaGlt 482
   ::::: ::::: ||| ||| ||||| ::::: ::::: :::::
376 CGGACATCGCGACAGTACGATTTGGCGGAGCGCTACATCAGCCAGCT 425
   ::::: ||| ||| ||||| ::::: ::::: ::::: :::::
482 rgtGlt.....ArgAlaIaIaAgtAgtAgtAgtAgt..... 491
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
426 TCCGTTCCCGCTGACCGCGCATGTACAAACCGCGAAATCAAGGATAG 475
   ||||| ||||| ||||| ::::: ::::: ::::: ||
492 .....ProAlaAsPrg.....AsPrgtAgtAlaIaHisAtr 501
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
476 ACAAAATATGAGCGCGGAGGATTTCGCGCAAGAAAMAC..... 518
   | ::::: ||||| ::::: ||| ::::: ||| ::::: |||
501 gLeuGltAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgt 518
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
519 .....CGCGCTTACACGACTACAAAGGCGTCMAAACAAATCATCAAC 560
   ||||| ||||| ::::: ::::: ||| ::::: ||| ::::: |||
518 InProLeuPrgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtA 534
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
561 CCGGCGTTGGCGGAGAACCAACCATGCTGCGCGCAACCACTCCCTCC 610
   ||||| ||| ||||| ||||| |||||
535 ProAla.....ArgAgtAgtAgtAgtAgtAgtAgt..... 544
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
611 CTCAGAGCGCGGGAAGCGGTATGGGCTGATTTCTTCGGCA..... 653
   ||||| ||||| ||||| ::::: ::::: ::::: :::::
545 ....AlaAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgt 560
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
654 .....ACGCTTATCCATGAC 671
   ::::: ::::: |||
560 aIProValProAsPrgtAgtAgtAgtAgtAgtAgtAgtAgtAgtAgt 576

```


TELEPHONE: 215-540-9200
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 302 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-113-921-3

alignment_scores:
 Quality: 107.50 Length: 166
 Ratio: 1.265 Gaps: 6
 Percent Similarity: 51.205 Percent Identity: 27.711

alignment_block:
 US-09-303-518D-569 x US-09-113-921-3 ..

Align seg 1/1 to: US-09-113-921-3 from: 1 to: 302

```

156 AGACCGCGCGCATCTGCGCAATATGCTGACGACGATGATCCG 205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
143 ArgGlnArgArgArgProProGlnAspSerSerGlyArgGlnArgArg 159
206 ACCCCAAACGGT.....CAAGCCGTTT.....TGGGAA 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
159 gProProGlnGlySerGlySerArgGlnArgArgGlyProProGlnGly 176
238 AGGGAAGAGCGGTTTGAACCTGCCCCGCGTTTTCAGAAACCGGA 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
176 eGlySerArgGlnArgArgArgProProGlnAspSerSerGlyArgGln 192
288 AGACATAGAACATGTTCAAGCGGTACACGCTGGGAAACATGTCAGC 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
193 ArgArgArgSerProGlnAspSerGly..... 201
338 AGGCTTTGACAAACAGAGGCGTCTATTCACGCGGCACATCGGC 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
202 .....GlyArgGlnArgArgArgSerProGlnAspSerGlyGlyArg 216
388 ACCTAGATTTGGCGGACGTACATCAACCGACGCTCCGTCGCGT 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
216 LlnArgArg..... 218
438 GAACCGCATGTACAAACCGCCGAATCAACGATGACAAATCATGTC 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
219 .....ArgThrProGlnSerSerSerGlyArgGlnArgArgArg 231
488 AGCGGCGCAG.....GTTTCGGCGCAAGAAACCGCGCTACGACG 531
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
231 gAlaHisGlnAspSerGlySerArgGlnArgArg.....ArgAlaHisGln 247
532 ATTCAGAGGGGTCAACCAATCATCAAGCGCTGCGGTGGCGCAACAG 581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
247 spSerSerGlyArgGlnArgArgArgGlnAspSerSerGlySerArg 263
582 CATGCTCTCCCGGACGACGTCCTCCCTCCCTCAAGAGGCGGGAGAG 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
264 GlnArgArgArgArgProProAspSerSerGlyArgGlnArgGlnArg 279

```

seq_name: /cgn2_6/plodata/1/laa/6B_COMB.pep:US-09-232-468A-8

seq_documentation_block:

; Sequence 8, Application US/09232468A
 ; Patent No. 6207165
 ; GENERAL INFORMATION:
 ; APPLICANT: AUDONNET et al.
 ; TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
 ; FILE REFERENCE: 454313-2230
 ; CURRENT APPLICATION NUMBER: US/09/232,468A
 ; CURRENT FILING DATE: 1999-01-05

NUMBER OF SEQ ID NOS: 54
 SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 404
 ; TYPE: PRT
 ; ORGANISM: Aujeszky's Disease Virus (NIA3 Strain)
 US-09-232-468A-8

alignment_scores:
 Quality: 103.00 Length: 305
 Ratio: 0.792 Gaps: 12
 Percent Similarity: 42.623 Percent Identity: 22.951

alignment_block:
 US-09-303-518D-569 x US-09-232-468A-8 ..

Align seg 1/1 to: US-09-232-468A-8 from: 1 to: 404

```

36 GCGAACCGCCATGACATCTGTTGACCGCGCTGCTCAATGCTCTCC 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
129 AlaProHisHisAlaAspValAlaAspProValArgGlyLeuHisValPr 145
86 TGCTGCCGCTTCTCTG...TCTGCACACGCTGGAAACCGGCTCGACAT 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
145 OHISGlyGlyArgAlaGlyAlaHisGlyGlyProArgAlaValGln 162
133 CTGGCGCTTTACCTTTAAAGAAAGACCGCGCGCATGCTGCCAATAT 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 rGlyProValAlaProAlaProGlyValAlaArgArg.....ArgArgGlnHis 176
183 GCGTCACGACAGCATGATCCGACCCCAACCGGTCAAGCCGTTTGT 232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
177 ProHisArgLeuHisGlyGlyAlaProArgGlyAlaArgValAlaProVal 193
233 CGGAACCGCAAAAGCGGTTTGGAACTTCCCCCGGCTTTTCAGAAA 281
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
193 gProArgGlyProAlaProHisValGlnValArgArgValLeuGlnArg 210
282 .....ACCGGAACATGTAACCAATGTTCAACGCGGTACACGG 320
210 rGlnLeuGlnAlaGlyArgGlyArgAspAlaLeuProAspAlaValLeu 226
321 CTGGAAACATGTGCAGCAGGCTTTGACAA..... 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
227 ProAlaAlaProAlaProGlyGlyGlyLeuValProGlnGlnArg 243
351 .....ACAGAAAGCGCTGCTATTCATCAGCCCG 378
243 gProAspAlaProAlaGlyProArgArgArgHisAlaValArgHisArg 260
379 CACATCGCAGCTACGATTTGGCGGACGCTACATCAGCCAGCA..... 422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
260 rOHValAlaValLeu.....GlyGlyLeuAlaGlyAlaProAlaProAla 274
423 ...GCTTCGTTCCCGCTGACCGCCATGTACAAACCGCCGAATCAAG 469
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
275 ProAlaProAlaProAlaGlyAlaArgAlaArgProGlyAspAlaArgAl 291
470 CGATGGA...CAAAATCATGACGCGGCGGAGGTTCCGCGCAAG... 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
291 ArgArgProProAlaArgAlaGlyAspAlaGlyProArgArgArgGly 308
513 ..AAAACCGCGCTACCATACGATACAGAGGTTCAAAATCATCAAGC 560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
308 rOHProHisAlaAlaThrProGlnAlaArgAspAlaAlaProProLeuArg 324
561 CCGGCTTCGGCGGCGGACAGACCATGCTCTCGCCGACAGCT..... 602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
325 ProAla...GlyArgArgAlaGlnArgValAlaAlaAlaArgGlyAla 340
603 .....CCCGCTCCCT 612
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[illegible]

US-09-248-335-26

alignment_scores:
 Quality: 100.00 Length: 276
 Ratio: 0.855 Gaps: 15
 Percent Similarity: 42.391 Percent Identity: 24.638

alignment_block:
 US-09-303-518D-569 x US-09-248-335-26 ..

Align seg 1/1 to: US-09-248-335-26 from: 1 to: 370

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117 AACCGGCTCGACATCTGGCGTTTACCT..TTTAAAGAGAGCCGCG 163
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78 LysTYRAlaLysGlnGlyAsnProLeuProAspTrpHisGlyArgAlaG1 94
164 GCGG.....CATGTCGCGCATATGCGTCAGGAGCGCATGATCCGAC 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
94 yAlaGlyValHisArgAlaValAlaAlaAspGlyGlyAlaGluLeuArg. 110
208 CCCAAAGCGTCAAGACCGTTTTCGGGAAGCGCAAAAGCGGTTTGA 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
111 .....ArgAlaGlnArgArgAspGly 117
258 ACTTGGCCCCGGGCTT..... 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
118 LeuGlnProArgLeuProAlaAlaHisProAlaGlnAlaGlnArgLnr 134
273 .....TTTCAGAAAACCGGAGAGACATAGAAAACATGTTCAAA 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
134 gGlnArgArgArgValGlnArgGlnGlyArgHisArgArgGln..... 148
310 GCGGTACAGCGCTGGGACATGTGACGAGCGTTTGACAAACAGAGAG 359
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
149 .....GlnArgArgArg 152
360 GGTGATTATCATCAGCCGACATCGGACAGTACATTTGGCGGAGCGT 409
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153 .....ValGlnArgGlnAlaArgCysGlyArgVal... 162
410 ACATCAGCCAGAGCTTCGCTCCGCTGACCGCCATGTACAAACGCGG 459
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163 .....ThrAlaG 165
460 AAAATCAAGCGATAGCAAAATCATGACGAGCGGAGGTTCCGGGCAA 509
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165 LysGlyIuProAspGlnGlyArgAlaGlnGlyGlyAspAlaGln 181
510 AGGAAAACCGGCGCTACGACATACAGGCGTCAACAAATCATCAAG 559
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
182 AlaVal.....ArgAlaGlnGlnGlnGlyProGlyGlnAla..... 193
560 CCCTGGCTTGGGCGGAAGCAACCATCGTCTCCGCGACAGCATCCCTCC 609
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194 .....AlaGlyHisLeuArgAlaAlaPro..... 201
610 CCTCAGAGAGCGGAGGAGCGGTATGGGTGATTTCTTGGGCAACCTGC 659
201 ..... 201
660 CTATACATGACGCTGGCGGCAAAAT..GGCAGACGTCAA...AGGCG 703
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
202 .....GlyGlyGlnHisValProGlyArgArgGlnLeuHis 214
704 TGAAGAACCTGTTTCTGCTGGAGAGCGCTGCTGGCGG.....ACAA 747
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214 sArgArgProVal.....AlaProAlaLeuArgGlyProPro 227
748 GGTTCGATTTCACATCCGCCCGCTCCAGAGGGAATGAAAGCGGAGCA 797
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227 rGleuArgProAlaLeuProHisValArgValProGlnGlnArgGln 243

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798 AGCCCATGATCCCGCGTGTCAACCGCAA...TGCCGATATTGATAC 844
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244 GlnValValAlaArgArgLeuArgProArgHisLeuGlnValArgGlns 260
845 GCGGTTTCGAGCAGATCTGTTAT 872
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260 ProAlaAlaProAlaValHisValHis 269

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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-083-590A-20

seq_documentation_block:

; Sequence 20, Application US/08083590A

; Patent No. 5786158

; GENERAL INFORMATION:

; APPLICANT: Artavanis-Tsakonas, S. et al.

; TITLE OF INVENTION: Therapeutic And Diagnostic Methods

; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESS: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/083,590A

; FILING DATE: 25-JUN-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mistock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 7326-015

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 790-9090

; TELEFAX: 212 869864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 256 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; US-08-083-590A-20

alignment_scores:

Quality: 97.00 Length: 275

Ratio: 0.815 Gaps: 19

Percent Similarity: 43.273 Percent Identity: 23.636

alignment_block:

US-09-303-518D-569 x US-08-083-590A-20 ..

Align seg 1/1 to: US-08-083-590A-20 from: 1 to: 2556

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2 TGTTCGTTTACAAATTCAGGCTGTTCCCTTTCGGAACGCCA..... 46
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89 CysAlaLeuGlyPheSerGly.....ProLeuGlyHisProLeuAs 103
47 .....TGCACATCTGTTGACCGCGCTCAATGCGTCTCCCTGC. 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
103 pAsnAlaCysLeuThr.....AsnProCysArgAsnGlyThrCysA 118
89 .....TGCCGCTTTCCTGTCGACACAGC 112
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196 .....HtsaenglVala1glYseTtYArg.cysValcYargAla1ehrHl 210
318 CGCGTGGGAACATGTGCAGCAGCGTTTGGACAACAACGAAGCGTCTCTAT 367
1 .....HtsaenglVala1glYseTtYArg.cysValcYargAla1ehrHl 210
210 S..ThrglyProAnaCysgluYargProTyrVal.....ProCysSer 223
368 TCATCAAGCGGCACATCGCAGCTACGATTTGGCGGAGCGCTACATCAGC 417
224 ProSer.....ProCysGlnAsn..... 225
418 CAGCAGCTTCGTTCCCGCTGACCGCCATGTACAAACCGCCGAAATCA 467
226 .....ProCysGlnAsn..... 229
468 AGCAGTAGACAAATATCATGCAAGCGGGCATTTGGCGGAAAGAAA 517
230 .....GlyglYthCysArgProThrGlyAspValThrHs1glucYs 243
518 CCGCGCTTACCAGCATCAAGGGGTCAACAATAATCATCAAAAGCCCTCGT 567
244 AlaCysLeuProGlyPheThrGlyAsn.....Cys.. 254
568 TCGGGCGCAACCAATCGTCTGCGCCGACAGCTCCCTCCCTCAGA 617
255 .....GluGluAsn1LeaSpaPcysProGlyAsnAsn.....CysYsA 268
618 AGCGCGGAACGCTATGCGGATTCCTTCGCAAACTCGCTATACA 667
268 snGlyglYalacYsVala1spGlyAla1snThrYranCysProCysPro 284
668 TGACGCTCGCGCAAAATTGGCACACGCTCAAAAGCGTGAAACCCCTGTT 717
285 ProGluThrPthrGlyGlnTyrCysThrGluAspVal...AspGluCysGl 300
718 TTCTGCTGCGAAGCGCTGC 736
300 nLeuMetProAsnAlaCys 306

seq_name: /cgn2_6/prodata/1/1aa/5B_COMB.pep:US-09-056-226-2
seq_documentation_block:
? Sequence 2, Application US/09056226B
? Patent NO. 6177614
? GENERAL INFORMATION:
? APPLICANT: Colasanti, Joseph J.
? APPLICANT: Sundaresan, Venkatesan
? TITLE OF INVENTION: Control of Floral Induction in Plants
? TITLE OF INVENTION: See Therefor
? FILE REFERENCE: CSH094-04A4
? CURRENT APPLICATION NUMBER: US/09/056,226B
? CURRENT FILING DATE: 1998-04-07
? EARLIER APPLICATION NUMBER: US 09/000,640
? EARLIER FILING DATE: 1997-12-30
? EARLIER APPLICATION NUMBER: US 08/804,104
? EARLIER FILING DATE: 1997-02-20
? EARLIER APPLICATION NUMBER: PCT/US96/03466
? EARLIER FILING DATE: 1996-03-15
? EARLIER APPLICATION NUMBER: US 08/406,186
? EARLIER FILING DATE: 1995-03-16
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 2
? LENGTH: 436
? TYPE: PRT
? ORGANISM: Zea mays
? US-09-056-226-2

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  Quality: 96.50
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  Length: 222
  Gaps: 10
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alignment_block:
US-09-303-518D-569 x US-09-056-226-2
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Align seg 1/1 to: US-09-056-226-2 from: 1 to: 436

[illegible]

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seq_name:/sgn2_6/ptodata/1/1aa/5A_COMB.pep:US-07-745-206A-13
seq_documentation_block:
; Sequence 13, Application US/07745206A
; Patent No. 5429921
;
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McGue, Ann
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: Human Calcium Channel Compositions and
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340 GCTTTGGAC.....AAACA 355
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1014 ArgSerSerGlyThrThrSerProGlySerHisThrValI ThrTParPr 1030
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354 CGAAGGCTGCTATTCATCACCGCACATCGGCAGCTAGCATTTGGCGC 403
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1030 oValGlyLeuLeuThrPValHisAlaHisThrIaGlnInProValSera 1047
      |||||LeuLeuThrPValHisAlaHisThrIaGlnInProValSera 1047
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404 GACGCTCATATGACGACAG.....423
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1047 rGaTgTTParPaSnsSerGlnArgMetGlnThrIleSerGlyThrSerLeu 1063
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424 .....CTTCGCTTCCGCTGACCGCATGTAC.....450
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451 .....AAACG.....CCGAATAATCAACGATAG 475
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476 ACAAAATCATGACAGCGGCGAGGTTCCGCGCAAGAAACCGCGCT 525
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526 ACACGAGTCACAGGGGTCACAAACAAATCATCAAGCCCTGCGTTGGCGCA 575
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1113 ..AlaIaProGlyLeu.SerSerHisThrAlaProCysSerVala. 1127
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576 AGCAACATCGTCCCTGC.....CCGACCACGTCCTCCCTCCCTC 613
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1128 ....ProProThrCysSerAlaAlaSerAlaThrThrSerProGlyThr 1142
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614 AAGAGGGCGGGGAAGCGTATGGG.....637
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1143 SerArgTrpSerPheSerTrpSerSerProAlaAlaSerProTrpLeuIle 1159
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638 .....TGCA 641
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1159 uArgTrpGlnCysAlaGlnThrArgProGlyThrThrLeuAsnThrTrpI 1176
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642 TTTTCTTCGGCAACCGCTATACCATGACGCTGGCGGCAAAATGTGCAC 691
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1176 LeThrPheSerLeuValSerLeuProLeuArgTrpArgSerThrTrpAsp 1192
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692 ACGTCAAAGGCGTGAAACCCCTGTTTTC.....GCTCGCAAGC 732
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1193 Cys.....CysPheThrLeuGlnProIleSerGly 1203
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733 CTGCCGGCGGACAGGTTTCATTTGCATTCGCATCCGCCCG.....772
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1203 rCysGlyThrPheTrpThrSerLeuThrPserValaIaProTrpTParGL 1220
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seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.dep:US-08-311-363-13

seq_documentation_block:
: Sequence 13, Application US/08311363
: Patient No. 5876958
: GENERAL INFORMATION:
: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Feldman, Daniel
: APPLICANT: McCue, Ann
: APPLICANT: Brenner, Robert
: TITLE OF INVENTION: Human Calcium Channel Compositions and
: TITLE OF INVENTION: Methods
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:

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[illegible]

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997 gAgtArGArGrPrOAlArGArGArGLeuArG...TryLysPrOThrIAlGlys 1013
340 GCTTGGAC.....AAACA 353
1014 ArgSerSerIAlThrThrSerProGlySerHisThrValIThrTrpArgPr 1030
354 CGAAGGCGTCATTCATCAGCGCGCCGACATCGGAGCGAGCTAGCATTTGGGCG 403
1030 oValGlyLeuThrValIHisAlaHisThrAlaGlnGlnProValSerA 1047
404 GAGCGTACATCAGCCAGCAG..... 423
1047 rGrArgTrpArgAsnSerGlnArgMetGlnThrIleSerGlyThrSerLeu 1063
424 .....CTTCGCTCCCGCTAGCCCGCATGTAC..... 450
1064 AlATrPrAlaValSerProGlnThrArgThrLeuLeuThrIleSerGlnCy 1080
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476 ACAAAATCATCAGCGCGGCGAGGTTCGCGCAAAAGAAAACCGCGCCT 525
1097 rPlsAlaLysGlnArgGlyArgAdAAdGTrpLysArgMetThrGly... 1112
526 ACAGCATCAAGGGGTGCACAAATCATCAAGCGCTGCTGGGCGA 575
1113 ...AlaIAlaProGlyLeu.SerSerHisThrAlaProCysSerValAla. 1127
576 AGCAACCATCGTCTGC.....CCGACACAGTCCCTCCCTCC 613
1128 ....ProThrTrpCysSerAlaAlaSerAlaThrThrSerProGlyThr 1142
614 AAGAGCGGGGAAAGCGTATGGG..... 637
1143 SerArGTrpSerPheSerTrpSerSerProAlaAlaSerProTrpLeuLe 1159
638 .....TGGA 641
1159 uArGThrGlnCysAlaGlnThrArgProGlyThrThrLeuAsnThrTrpI 1176
642 TTTCCTGGGCAACCTGCCATACATAGCGGTGGCGCAAAATGGCAC 691
1176 lEtIrnPheSerLeuValSerLeuProLeuAlaArgTrpArgSerThrTrpAsp 1192
692 ACGTCAAAAGCGTGAAACCCCTGTTTTCT.....GCTCGCAGAC 732
1193 Cys.....CysPheIrnLeuGluProIleSerGlyTh 1203
733 CTGCGTGGCGACAGGTTTCATTTGCACATCCGCCCG..... 772
1203 rCysGlyThrPheTrpThrSerLeuTrpSerValAlaProTrpTrpArgL 1220
773 .....TCCAGGCG 781
1220 euLeuSerArgSerLysGly 1226

seq_name: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:US-09-041-886-19
seq_documentation_block:
: Sequence 19, Application US/09041886
: Patent No. 623872
: GENERAL INFORMATION:
: APPLICANT: Bredesen, Dale E.
: APPLICANT: Rabinzadeh, Sharroz
: TITLE OF INVENTION: Propeptidic Peptides, Dependence
: OF INVENTION: Polypeptides and Methods of Use
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego

```

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STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-19

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alignment_scores:
Quality: 93.00      Length: 326
Ratio: 0.633       Gaps: 14
Percent Similarity: 45.092   Percent Identity: 23.620

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alignment block:
US-09-303-518d-569 x US-09-041-886-19 ..

Align seg 1/1 to: US-09-041-886-19 from: 1 to: 1312

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71 TCMAATGCTCTCCCTGCTGCGCTTCTGTCACACGCTGGGAAC 120
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588 oSerArgProSerArgProProSerHisProSerIaHis...GlySerP 604
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121 CGGCT.....CGACATCTGCGCTTTTACCTTTT 149
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604 roIaIaProValSerThrMetProLysArgMetSerSerGluGlyPro 620
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150 AAGGAAGACGCGCGCGCATGCT.....CGCCAAATGGGCTC 187
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621 ArgMetSerProLysAlaGlnArgHisProArgAsnHisArgValSer 637
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188 AGCGAGG.....CATGAATCCC 204
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637 aGlyArgGlySerIleSerSerGlyLeuGluPheValSerHis AsnPro 653
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205 GACCCCAAGCGTCACAGCGCTTTTGGCAAGCGCAAAAGCGGTTT 254
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654 ProSerGluAlaIaIaThrProProValAlaIaArgThrSerProSer 669
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255 GGAAC.....TGCCCGCGCTTTTCAGAAAC 283
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670 GlyThrTrpSerSerValValSerGlyValProArgLeuSerProLys 686
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284 CGGAAGCATGTAAC.....AATGTTCAAGCG 312
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686 HisArgProArgSerProArgGlnAsnSerIleGlyAsnThrProSer 703
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313 GTACACGCGCTGGGAACATGTGACAGCGCTTTGACAAACGAAAGCG 362
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seq_name: /cgn2_6/plodata/1/1aa/6b_comb.pep:US-09-025-819-2
seq_documentation_block:
Sequence 2, Application US/09025819
Patent No. 6225097
GENERAL INFORMATION:
APPLICANT: Obata, Shusui
APPLICANT: Nishino, Tokuzo
APPLICANT: Koyama, Tanetoshi
APPLICANT: Sato, Yoshihiro
TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: KENON & KENON
STREET: 1500 K Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,819
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435

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720 AlaMetProIleProIa.....Al 726
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463 AT.....CAAGCATAGACAAATCATCGAGC 491
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743 eArgIaIaLysAspSerArgLeuGlnAspGlnArgGlnAsnSerProIa 759
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578 .....CAACCATCTTC 589
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 251675
FILING DATE: 17-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Khalilian, Hourl
REGISTRATION NUMBER: 39,546
REFERENCE/DOCKET NUMBER: 10235/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-220-4200
TELEFAX: 202-220-4201
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-819-2

alignment_scores:
Quality: 91.50 Length: 328
Ratio: 0.704 Gaps: 17
Percent Similarity: 39.634 Percent Identity: 24.695

alignment_block:
US-09-303-518D-569 x US-09-025-819-2 ..

Align seg 1/1 to: US-09-025-819-2 from: 1 to: 331

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34 AlaserghisAlarprogluvalthralahisLeuValgl 50
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62 C.....CGCCCTGCTCAATGCTCTCCCTGCTGCTTTC 99
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50 uAlaglylyArgLeuArgProMetLeuValLeuAlaAlaArgL 67
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100 TGCTGCACACGCTGGAAACCGGCTCGGACATGCGCTTACCTTT 149
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67 euCysglytyrGlnGly.....AsnerHisValLeu..... 77
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78 .....LeuAlaAlaGlySerSerse 84
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200 ATCCGACCCCAACGCTCAACCGCTTTTTC..... 233
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234 .....GAAACGGCAACGCGGTTTGGAACTTGCCTCCGCG 269
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97 etLysAlaSerSerGlyAlaAlaLeuArgArgProThrPheValGln 113
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114 GlnValGlnArgAlaGlyArg.....Ar 121
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121 GLeuTroValArgAlaGlnLeuProAlaSerGlyGlyGlyLys.... 156
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355 GAAGGGCTGTATTCATCAGCCGACATCGGACAGTTCGATTTGGGCGG 404
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405 AGCTATCATCAGCCAGACAGCTTCCCTGCTGACCCGCTGTAACAAC 454
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148 ArgHisHisArgArgGlyArgGlyAlaAlaAlaSerArgAlaGln.... 162
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194 AlaglyAlaAspProAlaGlySerArgArgCysSerThrMetaIaMetAr 210
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530 C.....CATACAGGGGTCAACAAATCATCAAAAGCCCTGCTCG 570
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571 GCGAAGCAACCATGCTCTCCGACACGCTCCCTCCCTCAAGAGG 620
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226 lArgProArgHisArgGlnGlnLuarGArgArgArgPheProArgAlaGln 242
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621 CGGGGAAGCGGTATGGGTGATTTCTTGGCAAAACGCTCATTCATGA 670
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243 Ala.....As 244
671 CGCTGGCGGCAAAATTTGGACACGTCAAGGCGTGAACCCCTGTTTTC 720
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244 PalAlaGlyAspGlnGlnHisArgProArgArgArgGlyArgAlaArgL 261
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721 TGCTGGCAAG.....CCTGCTGGCGGCAAG..... 749
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261 euLeuGlyThrHisArgProGlyProAlaGlyArgGlyArgProGly 277
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750 TTTCGATTTCACATCCCGCGCTCCCAAGGGAATTAAGCGCAACAAG 799
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278 HisArgAlaGlyAspProAlaProProArgGlyAlaGlyArgProAr 294
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800 CCCATGATGCGCGCTGTTCAACCGCAATGCCGA 833
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seq_name: /cgn2.6/ptodata/1/aa/5A_COMB.pep:US-07-925-695-8
seq_documentation_block:
; Sequence 8, Application US/07925695
; Patent No. 5428145
; GENERAL INFORMATION:
; APPLICANT: OKAMOTO, Hiroaki
; TITLE OF INVENTION: NON-A, NON-B, HEPATITIS VIRUS GENOME,
; POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Beveridge, Degrandt, Wellacher & Young
; STREET: 1850 M Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/925,695
; FILING DATE: 19920807
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 287402/91
; FILING DATE: 09-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 360441/91
; FILING DATE: 05-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wellacher, Robert G
; REGISTRATION NUMBER: 20,331
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333 LysArgLysSerArgTyrPaspGluThrProAlaSerGlnMetGlyGly.. 348
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694 GTCAAGCGCGTGAACACCTGTTTTCTGCTGGCAACGCGCT..... 734
363 .....ProAlaMetGlnMetAlaThrProThrProGly 373
735 .....GCTGGCGGCAAGGTT 751
374 HistMetSerMetThrProGluGlnLeuGlnAlaThrPArgTyrPgluAr 390
752 TCGATTTCACATCCGCCCGTCCAGGAGGATTGAACGGCGCAACAGCC 801
390 ggluileaspolduargasnArProleuSerArgPglu..... 403
802 CATGATCGCCGCGTTCACACCCGCAATGCCGAATATTGATACGCGGTTT 851
404 .....LeuAspAlaMetPhe 408
852 TCCGACGACGATATCTGTTTATGTACACCG 881
409 ProGluGlyTyrIlyValLeuProProPro 418
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seq_documentation_block:
; Sequence 3, Application US/07977630
; Patent No. 5583038
; GENERAL INFORMATION:
; APPLICANT: Stover, Charles K.
; TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING
; TITLE OF INVENTION: DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gillilan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,630
; FILING DATE: No. 5583038ember 17, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Herron, Charles J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 469201-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-977-630-3

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Quality: 89.50      Length: 312
Ratio: 0.678      Gaps: 17
Percent Similarity: 42.308      Percent Identity: 23.718

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18 GluAlaIaIaArgGluLysArgAlaArgTyrGlyLeu..... 29
270 GTTTTCAGAAACCGAAGACATAGAACAAATGTTTC..AAAGGGTAC 316
30 .....ArgLysValThrAspLeuHisLeuGlyPheHisLysAlaIleG 44
317 ACGGCTGGGACAT..... 330
44 InProThrSerHisGlyGluAspAspHisTyrAlaArgLLeuArg 60
331 .....GTCCAGCAGGCTTTGCA..CAACACGAGGCGCTGCATTCATCA 373
61 ArgAlaIaIaGlnGluAlaLeuThrPgluSerArgGluGlnAlaValLeuAr 77
77 gValValHisArgGluSerLeuGlyThrIleArgAlaGlyLeu..... 91
412 ATGACGACGACGCTCCCTCCCGCTGACCGCCATGTCAACCGCGCA 461
92 .....AlaAlaThrValArgArgLysLysArgValThrProGlnArg 105
462 AATCAAGGATAGACAAATCATCAGCGGCGAG..... 497
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498 .GGTTGCGCGCAAGAAAAACCGCGC.....T 525
122 yGluHisSerValArgValLysArgAlaIaLacSerHisGluGlyLeu 139
526 ACCAGCATCAAGGAGTCAACAAATCATCAAGCGCGCG..... 566
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567 .....TTGCGCGCA..... 575
156 HisGlyArgLeuGlyArgAspArgGlyLeuHisAlaValGlnAsnH 172
576 .....AGCAACCATCGCTCGCCGACCA..... 599
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600 .....CGTCCCTCCCTCAAGAGG..... 620
189 IaThrArgSerValArgArgGlnValProIleArgArgLysAlaArgPro 205
621 .....CGGGGAAGCGCTATGGGTGCATT 643
206 ValArgCysLeuAspArgProArgThrArgGlyArgGluProAspAlaPr 222
644 TCTT.....CGGC 651
222 OleuAspAlaHisProArgSerSerLeuGlyValValGlnArgPheArg 239
652 AAACCTGGCTA.....TACCATGAC 671
239 alThrArgLeuAlaIaArgAlaIaAspSerGlySerGlnValHisAsp 255
672 GCTGGCGGCAAAATTGGCACA.....CGTCAAGCGCTGAADA 709
256 AlaSerAlaLeuAlaIaThrAlaHisGluArgArgAlaArgLysArgH 272
710 CCTT...GTTTTCGTCGCAAGCGCTGCGCGGACAGGTTTCGAT 756
272 sProGlnThrHisLeuSerArgLeuProAlaMetGlyAsnGlyLeuArgH 289

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332 TGCAGCAGCTTTGGACAACACGAGGGCTGATTCATACAGCCGCGAC 381
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910 SGIuArgSerArgHisHisArgArgLysProGluGluAlaThrG 927
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927 IuArgLysProArgArgHisArg..... 934
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540 GGTCAACAATCATCAAGCCCTGCGTTC..... 569
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570 .....GGCGCAAGCA 579
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1000 uValAlaGluLysGluSerAsnValValGluGlyAspLysGluThrArg 1017
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580 ACCATGCTCTGCCGACACGCT 602
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB pep: US-08-185-432-17

seq_documentation_block:
; Sequence 17, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Bussseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELETED PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 330
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrick, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

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; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2556 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-185-432-17

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Ratio: 0.761 Gaps: 20
Percent Similarity: 42.545 Percent Identity: 24.000

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47 .....TGCACATCTCTGTGACCGCCCTGCTCAATGCTCTCCCTGC 88
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89 .....TGGCGCTTTCCTGCTGCACACGC 112
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118 sPheLeuThrLeuThrGluThrLysCysArgCysPro.ProGlyThrPse 134
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113 TGGGAAA.....CCGCGCTCGA 129
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134 rGlyLysSerCysGlnGlnAlaAspProCysAlaSerAsnProCysAlaA 151
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151 snGlyGlyGlnCysLeuProPheGlnAlaSerTyrIleCysHisCysPro 167
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184 nLysProArgLeuCysArgHisGly.....GlyThrCys.... 195
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318 CGGCTGGAGACATGTGCAGCAGCGCTTTGGACAACAGAAAGGCTGAT 367
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210 s.ThrGlyProAsnGly..... 216
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217 .....TrrProTyrValProCysSe 223
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418 CAGCAGCTTCGTTCCCGGTGACCGCATGTACAAACCGCAAAATCA 467
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223 rProSer.....ProCysGlnAsn..... 229
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618 AGCGCGGAGAGCGGTATGGGTGATTTCTTCGCAAACTGCTATACCA 667
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268 snGlyGlyAlaCysValAspGlyValAsnThrTyraCysProCysPro 284
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668 TGACGCTGCGCGCAAAATTGGCACACGCTCAAGGCGTGAACCCCTGTT 717
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285 ProGlnThrPrlngLglnTyrcystHrcGluAspVal...AspLucysG 300
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seq_documentation_block:
; Sequence 2, Application US/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCF
; CURRENT APPLICATION NUMBER: US/09/600,776
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: JP P1998-011434
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: JP P1998-346198
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-600-776-2
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Quality:	88.50	Length:	282
Ratio:	0.665	Gaps:	17
Percent Similarity:	47.163	Percent Identity:	25.887

alignment_block:
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Align seg 1/1 to: US-09-600-776-2 from: 1 to: 1083

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104 TGCACACCGCTGGGAAA.....CCGCGTCGACATCT.....GGCG 138
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794 uAlaGlyProSerAlaProProArgAlaLeuGlu..... 805
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239 CGGCAAAAGCGGCTTTGGAACCTGCCCCGCGTTTTCAGAAAACGGAA 288
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806 .....GlyLeuArgLeuProProMetProThrAsnValProPro 818
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seq_name: /cgn2_6/plodata/1/iaa/5B_COMB.pep:US-08-726-306A-56
seq_documentation_block:
; Sequence 56, Application US/08726306A
; Patent No. 5938684
; GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1 Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; APPLICATION NUMBER: US/08/726,306A
; FILING DATE: 02-Oct-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 95/20080.4
```

FILING DATE: 02-Oct-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/009,832
 FILING DATE: 01-Jan-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Ph.D., Kathleen M.
 REGISTRATION NUMBER: 34,380
 REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 345-9100
 TELEFAX: (617) 345-9111
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 181 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-726-306A-56

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 Quality: 88.00 Length: 244
 Ratio: 0.967 Gaps: 12
 Percent Similarity: 37.295 Percent Identity: 25.820

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Align seg 1/1 to: US-08-726-306A-56 from: 1 to: 181

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102 TCTGACACAGCTGGGAACCGCGTCGACATGTGCGCTTTTACCTTTTAA 151
    ::::: ||| ::::: |||
4 AlaAlaGlyAlaGlyProLeuArg..... 12
152 AGGAAGACCGCGCGCATGTGCCAATATGCTCAGCAGCATGAAT 201
    ::::: ||| ::::: |||
13 .....ArgValHisArgGlnGlyAlaAlaAlaGly.....GlyA 24
202 CCCGACCCCAAAAGCGTCAAAACCGCTTTTGGGAAACGGCAAAAGCGG 251
    ::::: ||| ::::: |||
24 LagInProGlnProGly...GlyArgGlyCysGly..... 34
252 TTGGAAGTGGCCCGCGTTTTCAGAAACCGGAAGACATAGAAACA 301
34 ..... 34
302 TGTTCAAAGCGGTACACGGCTGGGAACATGTGCAGCAGCTTTGGACAA 351
    ::::: ||| ::::: |||
35 .....AlaAlaAla..... 37
352 CAGGAAGGCTGCTATTATCAGCGCGCACATGGCAGCATTTGGG 401
    ::::: ||| ::::: |||
38 .....AlaAlaGlyGlyProLeuArgGlyGly 46
402 CGGACGCTATACAGCCAGCAGCTCCGTCCTGACCGCGCATGTACA 451
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47 ArgAlaValArg.....AlaArgGlyProArgAspAla..... 57
452 AACCGCGCAAAATCAAGCGATGACAAATTCATGCAAGCGCGGCGGT 501
    ::::: ||| ::::: |||
58 .....ArgArgGlyAlaAlaProGlyArgGlyA 67
502 CGGCGCAAGGAACCGCGCTACACAGATACAGGGGTCAAACAAT 551
    ::::: ||| ::::: |||
67 LaArgSerAlaThrProGlyAla..... 74
552 CATCAAGCCCTGCTGGGCGCAAGCAACATGCTCTCCGCGACACG 601
    ::::: ||| ::::: |||
75 ...GlyAlaProAlaArgGlnHisArgAlaArgAlaProAlaProArg 90
602 TCCCTCCCTCAAGAAAGCGGCGGATGGT.....GGAT 642
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90 gArgGlyProAlaAlaArgGlyGlyArgGlyGlyGlyProAlaGlyA 107
643 TTTCTGGCAACCTGCTATACATGACGTCGGCGCAAAATGGCACA 692
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107 LaLeuArg.....AlaGlyGlyArgGlyGlyAla 116
693 CGTCAAGCGGTGAACCCCTGTTTCTG.....CTCGAAGCC 733
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117 ArgGlyProAlaGlnGlyAlaGlyAlaGlyAlaGlyValArgLeuPr 133
734 TGCCTGGCGGACAGGTTTCGATTTCCACATCCGCCCTCCACAGGGA 783
    ::::: ||| ::::: |||
133 Ala.....AlaProProGlyArgGlyGlyA 143
784 TTGAACGGCGCAAGCCCATGATGCCCGT 815
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143 rGAlaAlaArgProAlaProGlyLeuArgArg 153

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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-420-235B-33

seq_documentation_block:

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: Sequence 33, Application US/08420235B
: Patent No. 5801042
: GENERAL INFORMATION:
: APPLICANT: Chang, Yuan
: APPLICANT: Moore, Patrick S.
: TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
: TITLE OF INVENTION: SEQUENCES AND USES THEREOF
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/420,235B
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 45185-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 454 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-420-235B-33

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alignment_scores:
 Quality: 88.00 Length: 264
 Ratio: 0.746 Gaps: 14
 Percent Similarity: 44.697 Percent Identity: 21.970

alignment_block:

US-09-303-518D-569 x US-08-420-235B-33 ..

Align seg 1/1 to: US-08-420-235B-33 from: 1 to: 454

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12 ACAATTCAGGCTGTTCCCTTTCGAAACCGCATGACATCCTGTGA 61
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135 ThrValAspGlyValSerProProGluLysValAlaValAlaHisProLeuG1 151
62 CGCGCCCTGCTCAAAATGCTCTCCCTGCTGCGCGCTTCTCTGCTGCACAG 111
151 uGluLeuGlnArg.....LeuAlaArgAlaT 160
112 CTGGGAACCGCGCTCGACATCTGCGCTTTACCTTTAAAGAAAGACCG 161
160 hrProAspProAlaLeuThrArgGly.....Pro 169
162 CGCGCGCATGCTCGCAATATGCTGCAGCGACGATGATATCCGAC.... 207
170 .LeuGlnValLeuThrGlyLeuLeuArgAlaGlySerAspGlyAspArgA 186
208 .....CCCAAAACGCTCAAAAGCGCTTTT 231
186 laThrHisHisMetAlaLeuGlnAlaProGlyThrValAlaArgGlyGluSer 202
232 GCGGAA.....ACGCAAAAGCGCGTTTGACCTTCCCGCGCTT 272
203 LeuAspProProValSerGlnLysGly.....ProAlaAr 214
273 TTTCAGA...AAACCGGAAGACATAGAAACATGTTCAAGCGTTACAG 319
214 gThrArgHisArgProProProValAlaArgLeuSerPheAsnProValAsnA 231
320 GC.....TGGGAACATGTGCAGACGCTTTGCACAAACAC 354
231 laAspValProAlaThrTrp.....ArgAspAlaThrAsnValTrp 244
355 GAAGCGCTGCTATTTCATCAGCGCGACATGCGACGTAGCATTTGGCGG 404
245 SerGlyAlaProTyr.....TyrValCysValTyrGlnArgGlyG1 258
405 ACCTACATACGCCAGACGCTTCCGCTCCGCTACCGCCCATGTACAAAC 454
258 yArgGlnGlnAspAspTrpLeuProIleProLeuSerPheProGlnGlnP 275
455 CG..... 456
275 roValProProProProGlyLeuValPheMetAspAspLeuPheIleAsn 291
457 ...CCGAAATCAAGCATAGCAAAATCATGCAAGCGCGACGAGGTGCG 503
292 ThrLysGlnCysAspPheValAspThrLeuGlnAlaAlaCysArgThrG1 308
504 CGGC.....AAAGAAACCGCGCTACCGACATACAAAGGCGTCAAC 547
308 ngLyTyrThrLeuArgGlnArgValProValAlaIleProArgAspAlaG 325
548 AATCATCAAAAGCGCTGCTGCGG.....GAAGCAACCATCGTCTG 591
325 lIleLeuAspAlaValLysSerHisPheLeuGlnAlaCysLeuValLeu 341
592 CCGGAC.....CACGTCCCTCCCGC 611
342 ArgGlyLeuAlaSerGlnAlaSerAlaTrpIleArgAlaAlaThrSerPr 358
612 TCAGAAGCGCGGGAAGCGTATGGGTGATTTCTTCCGCG 651
358 oProLeuGlnArgHisAlaCysTrpMetAspValLeuGly 371

seq_name: /cgn2_6/ptodata/1/1aa/6b_COMB.pep:us-08-793-624-33
; seq_documentation_block:
; Sequence 33, Application US/08793624C
; Patent No. 6150093
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma Virus Sequences And
; FILE REFERENCE: 45185-C-PCI-US/JPM
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;; CURRENT APPLICATION NUMBER: US/08/793,624C
;; CURRENT FILING DATE: 1997-02-18
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 33
;; LENGTH: 454
;; TYPE: PRT
;; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-08-793-624-33
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alignment_scores:
  Quality: 88.00      Length: 264
  Ratio: 0.746      Gaps: 14
  Percent Similarity: 44.697      Percent Identity: 21.970
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alignment_block:

US-09-303-518D-569 x US-08-793-624-33

Align seg 1/1 to: US-08-793-624-33 from: 1 to: 454

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135 ThrValAspGlyValSerProProGluLysValAlaValAlaHisProLeuG1 151
62 CGCGCCCTGCTCAAAATGCTCTCCCTGCTGCGCGCTTCTCTGCTGCACAG 111
151 uGluLeuGlnArg.....LeuAlaArgAlaT 160
112 CTGGGAACCGCGCTCGACATCTGCGCTTTACCTTTAAAGAAAGACCG 161
160 hrProAspProAlaLeuThrArgGly.....Pro 169
162 CGCGCGCATGCTCGCAATATGCTGCAGCGACGATGATATCCGAC.... 207
170 .LeuGlnValLeuThrGlyLeuLeuArgAlaGlySerAspGlyAspArgA 186
208 .....CCCAAAACGCTCAAAAGCGCTTTT 231
186 laThrHisHisMetAlaLeuGlnAlaProGlyThrValAlaArgGlyGluSer 202
232 GCGGAA.....ACGCAAAAGCGCGTTTGACCTTCCCGCGCTT 272
203 LeuAspProProValSerGlnLysGly.....ProAlaAr 214
273 TTTCAGA...AAACCGGAAGACATAGAAACATGTTCAAGCGTTACAG 319
214 gThrArgHisArgProProProValAlaArgLeuSerPheAsnProValAsnA 231
320 GC.....TGGGAACATGTGCAGACGCTTTGCACAAACAC 354
231 laAspValProAlaThrTrp.....ArgAspAlaThrAsnValTrp 244
355 GAAGCGCTGCTATTTCATCAGCGCGACATGCGGACGTAGCATTTGGCGG 404
245 SerGlyAlaProTyr.....TyrValCysValTyrGlnArgGlyG1 258
405 ACCTACATACGCCAGACGCTTCCGCTCCGCTACCGCCCATGTACAAAC 454
258 yArgGlnGlnAspAspTrpLeuProIleProLeuSerPheProGlnGlnP 275
455 CG..... 456
275 roValProProProProGlyLeuValPheMetAspAspLeuPheIleAsn 291
457 ...CCGAAATCAAGCATAGCAAAATCATGCAAGCGCGACGAGGTGCG 503
292 ThrLysGlnCysAspPheValAspThrLeuGlnAlaAlaCysArgThrG1 308
504 CGGC.....AAAGAAACCGCGCTACCGACATACAAAGGCGTCAAC 547
308 ngLyTyrThrLeuArgGlnArgValProValAlaIleProArgAspAlaG 325
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548 AATATCATGAAGCCCTGCTCGGC.....GAAGCAACCATGCTCTG 591
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335 IuIleAlaSPAlaValysSerHisPheLeuGluAlaCyLeuValleu 341
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
592 CCCGAC.....CACGTCCCTCCCC 611
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342 ArgGlyLeuAlaSerGluAlaSerAlaTrpIleArgAlaAlaTrpSerPr 358
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
612 TCAGAGAGCGGGGAGGCGTATGGGTGATTTCTCGGC 651
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358 oProLeuGlyArgHisAlaCyStrpMetAspValleuGly 371

seq_name: /cgn2_6/ptodata/1/iae/PCTUS-COMB.pep:PCT-US95-10194-33

seq_documentation_block:
; Sequence 33, Application PC/TUS9510194
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in the City of New York
; APPLICANT: City
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10194
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-C-PCT/JPM/MS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-10194-33

alignment_scores:
      Quality: 88.00      Length: 264
      Ratio: 0.746      Gaps: 14
      Percent Similarity: 44.697      Percent Identity: 21.970

alignment_block:
US-09-303-518D-569 x PCT-US95-10194-33 ..
Align seg 1/1 to: PCT-US95-10194-33 from: 1 to: 454

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135 ThrValaspGlyValSerProProlGluGlyAlaValAlaHisProLeuG 151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
62 CCGCCCTGCTCAAAATGCTCTCCCTGCTGCCGCTTCTGTCGACAGC 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
151 uGluLeuGlnArg.....LeuAlaArgAla 160
112 CTGGGAACCGGCTCGACATCTGGCGTTTACCTTTAAAGAAAGCG 161
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160 hrProAspProAlaLeuThrArgGly.....Pro 169
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162 CGCGCCATCGTCCCAATATGCGTCAGCAGCATGAATCCCGAC.... 207
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170 LeuGlnValleuThrGlyLeuLeuArgAlaGlySerAspGlyAspArg 186
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208 .....CCCAAAACGGTCAAGCCGCTTTT 231
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
186 LathHisHisMetAlaLeuGluAlaProGlyThrValAlaArgGlyUser 202
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
232 GCGGA.....ACGCAAAAGCGGTTTGAAACTGCCCCCGCGTT 272
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
203 LeuAspProProValSerGlnGly.....ProAla 214
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
273 TTTTAGA...AAACCGGAACATAGAAACATGTTCAAGCGGTTCACG 319
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
214 gThrArgHisArgProProProValArgLeuSerPheAsnProValAsn 231
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
320 GC.....TGGGAACATGTGCAGCAGCGCTTTGACAAACAC 354
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
231 IAspValProAlaThrTrp.....ArgAspAlaThrAsnValTrp 244
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355 GAAGGCTGCTATTATCATCAGCGCGCATCGGACGTCATGTTGGCGG 404
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245 SerGlyAlaProTyr.....TyrValCyValTrpGluArgGlyG 258
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405 ACGCTACTACGACGACGACGCTCCGCTCCGCTACCGGCATGTACAAAC 454
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258 YArgGlnGluAspAspTrpLeuProIleProLeuSerPheProGluGlu 275
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455 CG..... 456
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275 roValProProProGlyLeuValPheMetAspAspLeuPheLeuAsn 291
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457 ..CCGAATCAAGCGATAGACAAATCATGCAAGCGGCGAGGTTGC 503
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292 ThrLysGlnCysAspPheValAspThrLeuGluAlaIaIaCysArgThrG 308
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504 CGGC.....AAAGCAAAACCGCGCCTACGACGATCAAGGGTCAAC 547
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308 nGlyTrpThrLeuArgGlnArgValProValAlaIleProArgAspAla 325
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548 AATATCATGAAGCCCTGCTCGGC.....GAAGCAACCATGCTCTG 591
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325 IuIleAlaSPAlaValysSerHisPheLeuGluAlaCyLeuValleu 341
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592 CCCGAC.....CACGTCCCTCCCC 611
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342 ArgGlyLeuAlaSerGluAlaSerAlaTrpIleArgAlaAlaTrpSerPr 358
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612 TCAGAGAGCGGGGAGGCGTATGGGTGATTTCTCGGC 651
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358 oProLeuGlyArgHisAlaCyStrpMetAspValleuGly 371

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seq_documentation_block:
; Sequence 4, Application US/09449285A
; Patent No. 6313280
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie
; TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
; FILE REFERENCE: 2676-4232US
; CURRENT FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: PCT/EP98/03193
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 97201645.5
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
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LENGTH: 950
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-449-285A-4

alignment_scores:
 Quality: 88.00 Length: 342
 Ratio: 0.591 Gaps: 18
 Percent Similarity: 43.567 Percent Identity: 23.099

alignment_block:

US-09-303-518D-569 x US-09-449-285A-4 ..

Align seg 1/1 to: US-09-449-285A-4 from: 1 to: 950

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354 ProgluValArgProgluIuIysLeuAlaThrProSerIysProGlyLeuSe 370
104 T.....
370 rProSerIysTyIysTrpIysAlaSerSerProSerAlaSerSerSers 387
105 .....GCACAGCCTGGGCAACCGCGCTGGAGCATCTGCGC 137
387 erSerPheArgTrpGlnSerGluAlaIleIysSerIysAspHisThrSerGln 403
138 GTTTTACCTTTTAAAGAGACGCGCGGCATCTGCCAATATGCTGTC 187
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404 LeuSerProValProSerArgProThrSerGlyAspArgPro...AlaG1 419
188 AGGAGGACATGAAATCCGACCCCAAAACGTCACAAACCGCTTTTGGCGAA 237
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419 yGlyProSerSerLeuIysProLeuPheGlyGluSerGlnLeu..... 433
238 ACGGCAAAAGCGGTTTGGAACTTGCCCGCTTTTTCAGAAACCGGA 287
434 .....SerAlaTyIysValIysSerArgThrIlys 443
288 .....AGACATGAAACAATGTT.....CAAG 310
444 IleIleArgArgArgIysAsnThrSerIleProGlyAspIysLysAsnSe 460
311 CGGTACACGCGCTGGAAACATGTCACACGCTTTGGACAAACGCAAGG 360
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460 rProThrThrAlaThrThrSerIysAsnHisLeuThrGlnArgArgG 477
361 CTCTATTTCATACGCGGCACATCGGACGTACGATTGGGCGGACGCTA 410
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477 InAlaLeuArgIysLysAsnSerProValLeuArg.....LysThrPro 491
411 CATCAGCAGCAGCTTCGCTT.....CCGCGC 436
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437 TGACCGC...CATGTACAAACCGCGCAAAATCAAGCATAGACAAATC 483
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484 ATGCAGCGCGGCAAGGTTGCGGCAAGAAACCGCGCTTACCAGACAT 533
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522 IsMetGlyIleProProSerAsnLysValIleLysThrArgTyArgIle 538
534 ACAAGGGGTCAACAATCATCAAGCGCTTCGCGGCGCAACCAACCA 583
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539 ValIys.....LysThrProSerSerSerPheGly..... 548
584 TGCTCTCGCCGACACGCTCCCTCCCTCAAGAGAGCGGAGGAGCGCTA 633
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549 AlaProSerPheProSerSerLeuProSer...TyrArgLysArgArgI 564
634 TG..... 635

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564 LeProLeuSerArgSerLeuValLeuAsnArgLeuArgProAlaIleThr 580
636 GGTGATTTCTTCGCAAAACCTGCTATACCATGACGCTGGCGCAAAAT 685
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581 GlyGly..GlyLysAlaIleProProGlyThrPro...ArgTrpArgAsnLys 595
686 TGGCACACGTCAAAGCGGTGAAAACCTGTTTTCGTGCAAGCGCTG 735
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
596 GlyTyI.....ArgCy 599
736 CCTG.....GCGACAGATTGATTTGCA 761
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
599 sIleGlyGlyValLeuTyIysValSerAlaAsnLysLeuSerLysThrS 616
762 CATCCGCCCCGTCAGAGGGAATTTGAACGCGACCAAGGCC...ATGATG 808
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616 erSerArgProSerAspGlyAsnArgThrLeuLeuArgThrGlyArgLeu 632
809 CCGCGCGTTCACACCGCAATGCCGATATTGGATACGCCGTTTCCGACG 858
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633 AspProAlaThrThrCysSerArgSerLeuAlaSerArgAlaIleGlnr 649
859 CAGTATCTGTTTATGTACAACCGCT 883
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649 gSerLeuAlaIleIleArgGlnAla 657

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seq_documentation_block:

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; Sequence 431, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Manjand-Wikios, Shalina
; APPLICANT: Cao, Hui
; APPLICANT: Tsongalis, John
; APPLICANT: Drenkard, Eliana
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 431
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-431

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alignment_scores:
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 Ratio: 1.087 Gaps: 11
 Percent Similarity: 40.404 Percent Identity: 26.768

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Align seg 1/1 to: US-09-199-637A-431 from: 1 to: 162

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169 GCGAGCATGATCCGACCCCAAAACGTCACAAACCGTTTTCG..... 233
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6 GlyArgHisHisGly...ProValArgCysGlnGlnArgArgCysHisLe 21
234 .....GGAACGCAAAAGCGGTTTGGAACTTGCCCGCGCGGCTT 273
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21 uProGlyGlyLysArgGlyArgArgArg..... 30
274 TTCAGAAACCGAGACATAGAAACAATGTTCAAGCGGTACAGCGCTG 323
30 ..... 30
324 GGAACATGTGCACAGCTTTGGACAACAGAAAGGCTGATTCATCA 373
31 .....ArgAlaGlyGlyAlaGlnAlaArgSerProAlaLeuArgAs 44
374 CCGCCGACAT.....CGGCACGTACGATTTGGCGGACGCTAC 411
44 pProAspHisProValAspGlyArgHisLeuGlnLysArgCys.... 59
412 ATCAGCCACAGCTTCCTCCGCTGAC.....CGC 443
60 .....ProAlaArgGlnValProAlaAspProGlyAlaAlaGlnLysArg 74
444 CATGTACAAACCGCGAAATATCAAAACGATAGACAAATCATGACGGCG 493
75 HisLeuLeuCys.....HisProGlnPro 82
494 GCGAGGTTCGCGCAAGAAACCGCGCTACCGACATACAAAGGCT. 542
82 oProGlyCysArgGlyGlyThrGlyArgProValArgHisGlyProGlyG 99
543 .....CAACAAATCATCAAAAGCCCTGCGTGGCGGCAAGC 578
99 LysGlnProGlnGlnPheGlnLeuGlnProProAlaArgThrArgArg 115
579 AACCATTCCTCTCCGACACGCTCCCTCAAGAGCGGGAGAG 628
116 AlaHisGlyHisAla.....GlyLeuProAspArgArgArgGly 129
629 GCGATGCGTGATTTCTTCGCAACCTGCTATACATGAC..... 671
129 yHisAlaThrArgLeuValArgArg...CysAlaSerHisArgAsnHisA 145
672 .....GCTGGCGGCAAAATGCGCAACGCTCAAGGGGT 704
145 rGArgArgLeuArgAlaGlySerAlaGlyAlaArgSerAspArg 159

seq_name: /cogn2_6/ptodata/1/laa/6B_COMB.pep:US-08-861-774E-90

seq documentation block:
; Sequence 90, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
; APPLICANT: Waters, Barbara
; APPLICANT: Miao, Vivian
; APPLICANT: Ho, Yap
; APPLICANT: Tong, Seow
; TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
; FILE REFERENCE: 9993-006
; CURRENT APPLICATION NUMBER: US/08/861,774E
; CURRENT FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Clone ps24
US-08-861-774E-90

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alignment_scores:
  Quality: 87.00      Length: 282
  Ratio: 0.713       Gaps: 21
  Percent Similarity: 43.262   Percent Identity: 25.532

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alignment block:
US-09-303-518D-569 x US-08-861-774E-90
Align seq 1/1 to: US-08-861-774E-90 from: 1 to: 396

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19 AGCTGTTCCTCCCTTTGCAACCGCCATGCATCTGTGACCGGCT 68
101 LysLeuThrProProGlyHisValLeuProAspLeuArgLeuThrValLe 117
69 G.....CTCAATGCTCTCCCTGCG 88
117 uGlyGlyGlnThrLeuPheAlaGlnAspValAlaAspPheArgArgLeu 134
89 TCCCGCTTCCTCTGTCACACAGCTGGAAACCGGCTCGGA..... 129
134 LserLeuAsnGlyLeu.....LeuAlaAsnArgLeuGlyThrSerGlu 148
130 .....CATTCGCGCTTTTACCTTTAAAGAAAGCCGCGCGG 167
149 ThrGlyLeuPheArgLeuAlaPheLeu.....AspArgGlnThr 161
168 CATCTTCGCGCAAT..ATTCGTACAGCAGCATGATCCGACCCCAAA 214
161 rProLeuAlaAsnGlySerThrGlnAlaGlyThrGlnValProAspLys 178
215 CGGTCAAAAGCCGTTTTCGCGAAACGGCAAAAGCGGTTTGAACCTTGC 264
178 hVal...ValLeuPheAspArgLys.....GlyValGlnLeuAla 190
265 .....CCGCG 269
191 ProGlyAsnValGlyGlnLeuGlyValArgSerArgGlyLeuProGly 207
270 GTTTTCAGAAACCGAGACATAGAAACAATGTTCAAGCGGTACAG 319
207 YThrThrArgArgProGlyLeuThrSerGlnArgPheLeuThrSerLys 224
320 GCTGGGAACATGTGCACAGCGCTTGGAC.....AAA 351
224 LysAspAspArgValArgThrPheLeuThrGlyAspLeuGlyArgMetArg 240
352 CAGCAAGGCTGCTATTCATCAGCGCCGACATGCGACGATAGAT..... 396
241 AspAspGlyCysLeu.....GlnHisCysGlyArgLeuAspSerGly 254
397 .....TTGGCGGACGCTTACATCAGCCAGCAGCTTCGCTCCGC 436
254 nValLysIleArgGlyHisArgIleAlaMetGlyGlnLeuGlnPheLeu 271
437 TGACCGGCATGTACAAACCGCGAAATATCAAGCATAGCAAAATCATG 486
271 eu.....ArgThrCysAspGlyValSer 278
487 CAGCG.....GGCAGGTTTCGCGCAAGAAAC..... 519
279 GlnAlaValAlaIleAlaArgProHisSerAspGlyGlnThrArgLeu 295
520 .....CGGCTTACAGCATACAGGGGTCAAAACAATCATCAAG 559
295 eAlaLysPheValProThrGlnLysSerAlaIleAsp.....ValSer 310
560 CCGTCGCTG.....GGCAAGCAACCATCTGCTCCGCGACAC 600
310 eThrLeuArgHisLeuLeuGlyLys.....LeuProGlnHis 322
601 ..GTCCCTCC.....CCTCAAGAGCGG 623
323 MetIleProSerAlaPheValArgLeuAspGlyValPro.LysAsnAla 339
624 GGAAGCGCTATGGGTGATTTCTTCGCAACCGCTATACCA 667
339 sGlnLysValAspTrp.....AlaAlaLeuProAlaPro 350

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seq_name: /cgn2_6/prodata/1/iaa/5A_COMB pep:US-07-918-023-2
seq_documentation_block:
Sequence 2, Application US/07918023
Patent No. 5427934
GENERAL INFORMATION:
APPLICANT: Zimmermann, Thomas
APPLICANT: Robins, Karen
APPLICANT: Birch, Olwen
APPLICANT: Bohlen, Elisabeth
TITLE OF INVENTION: GENETIC ENGINEERING PROCESS FOR THE
PRODUCTION OF S-(+)-2,2-DIMETHYLCYCLOPROPANECARBOXAMIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fisher, Christen & Sabol
STREET: 2000 M Street, N.W., Suite 590
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,023
CLASSIFICATION: 435
FILING DATE: 19920724
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: CH 2247/91
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Marsh, Virgil H.
REGISTRATION NUMBER: 23,083
REFERENCE/DOCKET NUMBER: LP 1521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2000
TELEFAX: (202) 659-2015
TELEX: 248748
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PUBLICATION INFORMATION:
DOCUMENT NUMBER: IE 9224406
FILING DATE: 23-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 426
PUBLICATION INFORMATION:
DOCUMENT NUMBER: JP 198717/92
FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 426
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PL P 295408
FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 426
PUBLICATION INFORMATION:
DOCUMENT NUMBER: SU UNKNOWN
FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 426
PUBLICATION INFORMATION:
DOCUMENT NUMBER: CS PV2323-92
FILING DATE: 24-JUL-1992
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 426
PUBLICATION INFORMATION:
DOCUMENT NUMBER: HU P9202439
FILING DATE: 24-JUL-1992

RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 426
US-07-918-023-2

alignment_scores:
Quality: 86.50 Length: 297
Ratio: 0.698 Gaps: 15
Percent Similarity: 41.751 Percent Identity: 23.569

alignment_block:
US-09-303-518D-569 x US-07-918-023-2 ..

Align seq 1/1 to: US-07-918-023-2 from: 1 to: 426

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71 TCAATGCTCTCCCTGCTGCTGCTTCTGTCGACAGCTGGGAAC 120
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98 AProArgProSerProHisGly.....ArgCysHisArgGlyAlaG 112
121 CGGCTGGACATCTGGCGTTTAACTTTAAAGGAAGACCGCGCGCAT 170
||| :||| ||| ||| |||
112 InAlaAla.....ArgGlyArg...ArgArgHis 120
171 GCTGCCCAATATGCTGACGACGATGATCCGACCCCAAAAGCTCA 220
||| |||:||||| :|||
121 ProGlyInAlaAlaAspArgArgArgGlyArgProProSerArg 137
221 AAGCGTTTTTGGCGAAAGCGCAAAAGCGGTTTGAACCTGCCCCGC 269
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137 GAspHis.....CysProArgG 143
270 ..GTTTTCAGAAACCGGAACATAGAACAAATGTTCAAGGGGTACA 317
:|||||: :|||: |||||
143 InProLeuAlaArgProAlaMetAlaArgGlyLeuValGln..... 156
318 CGGCTGGGAACATGTGCACGACGCTTGGACAAACACGAGGCTGCTAT 367
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157 ArgLeuGlyArgGlyHisGlyGlyValAlaValLeuArgIleAlaGly 173
368 TCATGACCGCGCATCGGACGCTACGATTTGGCGGACGCTACATGAC 417
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173 SerLeuHisArgGlyLeuHisProLeuSerIleGlyArgGlnArgHis 190
418 CAGGAGCTTCC..... 428
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429 .....GTTCCGCGTACCGGCGCAT.....GTACAAACCGCGCAAAA 463
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207 GlyArgValAlaProGlyProHisArgProAspGlyAlaGlnCysArgGly 223
464 TCAAGCGATAGACAAATCAT.....GCAGCGGGGCGAGG 498
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223 SerGSerHisAlaArgGlyHisArgArgGlyGlyProAlaGlyProGly 240
499 GTTCGCGGCAAGGAAACCGCGCTACACGATGCAACGAGGTCGAAACA 548
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240 LysInProValGlnArgAlaArgLeuSerGlyHisAspAlaAlaArgIle 256
549 AATCATCAAAAGCGCTGCTGCGGCGAAGCAACGATGCTGCTCGGACG 598
:|||||: |||: |||
257 LeuArgProAlaArgProGlyHisGlyProAlaMetGlyThrGlyArgArg 273
599 ACGTCCCTCCCTCC.....TCAAGAA 618
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273 CysProLeuProProGlyGlyAlaGlyArgGlyGlyGlyAlaAlaArg 290
619 GCGCGGGAAGCGGTATGGGTGATTTCTCGGCAACGCTCATACCAT 668
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290 roGlyGlyGlnAlaArgAlaGlyGlyProLeuSerArg...Cys.....His 303
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669 GACGCTGGCGCAAAATT.....GGCACGTCGAAG 700
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334 .....ProArgAlaArgArgValAspArg 341

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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-337-602-3

seq_documentation_block:
; Sequence 3, Application US/08337602

; Patent No. 5623051

; GENERAL INFORMATION:

; APPLICANT: Catterall, William A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING

; TITLE OF INVENTION: FOR PRESYNAPTIC CALCIUM CHANNEL BLOCKERS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98042-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/337,602

; FILING DATE: 10-NOV-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 32,629

; REFERENCE/DOCKET NUMBER: 920010.602

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; TELEX: 3723836 SEEDANDBERRY

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 434 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-337-602-3

alignment_scores:

Quality: 86.50 Length: 233

Ratio: 0.779 Gaps: 11

Percent Similarity: 47.639 Percent Identity: 23.176

alignment_block:

US-09-303-518D-569 x US-08-337-602-3 ..

Align seg 1/1 to: US-08-337-602-3 from: 1 to: 434

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154 GAAGACCGCGCGCGCATGTCGCCAATATGCGTCAGCGAGCATGAAATCC 203
      |||:::|||||
85 GluGluArgLysLeuArgPheAlaThrThrArgHis.....LeuArgPr 98
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204 GCAAGCCCAAAACG.....GTCAAGCCGTTTGGGG 235
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seq_name: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:US-08-558-135-3

seq_documentation_block:
; Sequence 3, Application US/08558135

; Patent No. 6090631

; GENERAL INFORMATION:

; APPLICANT: Catterall, William A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING

; TITLE OF INVENTION: FOR PRESYNAPTIC CALCIUM CHANNEL BLOCKERS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

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98 oAspMetLysThrHisLeuAspArgProLeuValValGluLeuGlyArg 115
236 AAAGCGCAAAAGC.....GTTTGGAACTTCCCGCGGTTTTCAGA 279
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115 spGlyAlaArgGlyProValGlyLysAlaArgProGluAlaGlu 131
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280 AAACCGCAAGCATGAAACAATGTCGAACCGGTACACGGCTGGAGACA 329
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132 AlaProGluGlyValAspProProArgArg.....HisH 143
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330 TGTGAGCAGCGCTTTGGACAAACAGAGCGTGTATTATACACCGCG 379
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143 sArgHisArgAspLysAspLys.....ThrPro 153
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380 ACATGCGAGCTAGCATTTTGGGCGGAGCTATACATCAGCAGACTCCG 429
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226 HisArgAlaHisArgHisLysGlnAspProSerLysGluCysAlaGlyAla 242
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647 TCGCAAAACCTGCTATACCATGACGCTGCGCGCAAAATGCGACAGTC 696
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,135
FILING DATE: 13-NOV-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.602C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-558-135-3

alignment_scores:
Quality: 86.50 Length: 233
Ratio: 0.779 Gaps: 11
Percent Similarity: 47.639 Percent Identity: 23.176

alignment_block:
US-09-303-518D-569 x US-08-558-135-3

Align seg 1/1 to: US-08-558-135-3 from: 1 to: 434

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85 GUGUAGUGUAGUGUAGUGUAGUGUAGUGUAGUGUAGUGUAGUGU 98
204 CGACCCCAAAACG.....GTCAAGCGCTTTTGGCG 235
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98 oaspmkelystnHLSLeuAspargProLeuValValGluLeuGlyArg 115
236 AAACGCAAAAGC.....GCTTGAACCTTCCCGCGCTTTTACA 279
:: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
115 spGLYAlaArgIyProValGlyGlyAlaArgProGluAlaAlaGlu 131
280 AAACGCAAAAGC.....GCTTGAACCTTCCCGCGCTTTTACA 329
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
132 AlaProGluGlyValAspProProArg.....HSHI 143
330 TGTGACAGAGCTTGGACAAACGAAAGGCTCTATTTCACGCCGC 379
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143 sarGHisArgAspIyAspIy.....ThiPro 153
380 ACATGGCAGCTACGATTGGCGGAGCGCTACATCAGCGAGCTCCG 429
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153 IaaIaGlyAspGlnAsparg,AlaGluAlaProIyAlaGlySer.Gly 169
430 TTCCGCGTACGCGCATGTACAAACCGCGCAATCAACGATAGACAA 479
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169 IupProGlyAlaArgIyGluArgProArgProHisArgSerHisSerIy 185
480 AATATGCGAGCGGCGAGGCTTCCGCGCAAGGAAACCGCGCTACCA 529
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186 GluIaaIaGlyProProGluAlaArgSerGlyArgGly..... 200
530 GCATACAAAGGGGTCAAAATATCATCAAGCCTCGCTTGGCGGAGCA 579
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201 .....ProGlyProGluGlyArgArgH 209
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209 IshaArgArgGlySerProGluAlaAlaGluArgIyProArgArg 225
618 AGCGGGGAGAGCGCT.....ATGGGTGATTTCT 646
226 HisArgAlaHisArgHisGlnAspProSerIyGluCysAlaGlyAla 242
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seq_name: /cgn2_6/ptodata/1/aa/5A.COMB.pep:US-08-455-543A-48
seq_documentation_block:
; Sequence 48, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 238-0999
```

TELEFAX: (619)238-0062
 : INFORMATION FOR SEQ ID NO: 48:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2237 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : FRAGMENT TYPE: internal
 : US-08-455-543A-48

alignment_scores:
 Quality: 86.50 Length: 233
 Ratio: 0.779 Gaps: 11
 Percent Similarity: 47.639 Percent Identity: 23.176

alignment_block:
 US-09-303-518D-569 x US-08-455-543A-48 ..

Align seg 1/1 to: US-08-455-543A-48 from: 1 to: 2237

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807 OASRPETHSTHNLSEUASPARGPRLAUVALAIGLUENGLYARGA 824
236 AAACGGCAAAAGG.....GGTTGAACTGCCCCCGCGTTTTCAGA 279
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918 ISHISATGARGGLYSEPRROGLIUALAIGLALARGIUPROARGARG 934
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935 HISARGALAHISARGHISGLINAPPROSERLYGLUCYSALIGLYALAY 951
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seq_documentation_block:
 : Sequence 48, Application US/08223305C
 : Patent No. 5851824

GENERAL INFORMATION:
 : APPLICANT: Harpold, Michael
 : APPLICANT: Ellis, Steven
 : APPLICANT: Williams, Mark
 : APPLICANT: Feldman, Daniel
 : APPLICANT: McCue, Ann
 : APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 : NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
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 : STATE: California
 : COUNTRY: USA

ZIP: 92101-2926
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/223,305C
 : FILING DATE: April 4, 1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/868,354
 : FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/745,206
 : FILING DATE: 15-AUG-1991
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/620,250
 : FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/482,384
 : FILING DATE: 20-FEB-1990
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/603,751
 : FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: WO PCT/US89/01408
 : FILING DATE: 04-APR-1989
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/176,899
 : FILING DATE: 04-APR-1988

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TELEFAX: (619)238-0062
 : INFORMATION FOR SEQ ID NO: 48:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2237 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : FRAGMENT TYPE: internal
 : US-08-223-305C-48

951 sglvlnarlgarlgalaarghlsarglglvlyproalarglaaglyproalarg 968
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Sequence 47: Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:

LENGTH: 2339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-47
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Ratio: 0.779 Gaps: 11
Percent Similarity: 47.639 Percent Identity: 23.176
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968 luAlaIgluSerGly.....GluGluProAlaIArgArghls 979
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Mon Jul 1 09:26:08 2002

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Page 38

980 ArgAlaArgHisLysAlaGlnProAlaHisGluAlaValGluLys 994
